

Serial No. 09/807,946  
Amendment Dated November 30, 2005  
Reply to Office Action of September 23, 2004

### REMARKS/ARGUMENTS

This response to the Office Action of September 23, 2004 is filed concurrently with a Petition to Revive an Unintentionally Abandoned Application and the required statement. Entry of this amendment and reconsideration of the restriction is respectfully requested. Claims 1-15, and 19-29 are pending. Claims 1, 3-7, 9-11, 19, 23, 26, and 28 have been amended. Claims 1, 3, 4, 5, and 6 are amended to elect one polynucleotide sequence for examination. Claim 2 is cancelled based on the amendment to claim 1. Claims 16-18, and 30-35, directed to non-elected inventions, are cancelled. Applicant reserves the right to pursue the content of the cancelled and amended claims in continuing applications. Claims 6, 7, 11 and 26 are amended to put the claims in proper multiple dependent claim format. Claims 6, and 23 are amended to correct typographical errors. Claims 9, 10, 26, and 28 are amended to correct antecedent basis. Claims 19 and 23 are amended to replace "inducing expression" with "expressing". No new matter has been added by these amendments. Support for all amendments is found in the claims and throughout the specification as originally filed.

#### Claim Objection

Claims 6-35 were objected to under 37 CFR 1.75(c) as being in improper form.

Claims 6, 7, 11 and 26 are amended to replace "any of" with "any one of", as recommended by the Examiner, to put the claims in proper multiple dependent claim format. Applicants thank the Examiner for the recommendation.

#### Election/Restrictions

The claims as originally filed have been restricted into three groups, and Applicant is further required to select one sequence for examination.

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Applicant hereby elects with traverse to prosecute the claims of Group I and expressly reserve the right to file divisional applications or take other such appropriate measures to protect the inventions in the remaining claims. Applicants further elect SEQ ID NO: encoding SEQ ID NO: with traverse.

Applicant respectfully traverses the restriction of Group I and Group III. The Action asserts Group III is drawn to a probe, and effectively asserts that Group III is distinct from Group I, requiring different searches. The Action does not provide any assertion that Group III is independent of Group I, and does not show separate classification, and therefore does not fulfill the requirement of a showing that the restricted groups are independent AND distinct, as required by 35 USC 121, as described in MPEP 802 and 803, or that examination of both groups, even if independent and distinct, pose a serious burden on the examiner (MPEP 803). Further, Applicant believes this description of the claims of Group III improperly imposes a limitation not recited in the claims, the limitation that the polynucleotides could be used only as probes. Additionally, Applicant believes that the searches required for examination of Group I and Group III are essentially identical, and therefore do not pose a serious burden on the Examiner. Applicant respectfully requests reconsideration of the restriction. If this restriction is made final, Applicants respectfully request that the Examiner further demonstrate and clarify the basis of the requirement for the record.

The Action further requires the election of one corresponding pair of DNA and amino acid sequences. Applicant elects SEQ ID NOS: 5 and 6 for search and examination. Due to the restriction requirement, Applicant has amended the claims to recite only SEQ ID NOS: 5 and 6. Applicant respectfully request that the Examiner consider also searching and examining SEQ ID NOS: 7 and 8 in conjunction with the sequences elected above. Applicant provides Appendix A, which demonstrates that SEQ ID NOS: 6 and 8 have greater than 99% sequence identity to each other, and differ in length by only one amino acid residue. A GAP

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alignment of SEQ ID NOS: 5 and 7 is also provided, demonstrating that these sequences have greater than 99% sequence identity to each other, and have similar lengths (720 and 767 nucleotides respectively). Therefore, Applicant requests that the Examiner consider searching and examining these sequences concurrently in the present application, as provided for in MPEP 803.04.

### CONCLUSION

Applicants hereby elect to prosecute the claims of Group I, with SEQ ID NOS: 5 and 6, with traverse, and respectfully request reconsideration of the restriction of Groups I and III. Applicant further request that the Examiner reconsider the requirement to select one sequence for examination, in particular Applicant requests that the Examiner consider searching and examining the additional sequences of SEQ ID NOS: 7 and 8, in light of the evidence provided in Appendix A. It is not believed that any extension of time is required. However, in the event that additional extensions of time are necessary to allow consideration of the paper, such extensions are hereby petitioned under 37 CFR § 1.136(a) and any fee required therefore is hereby authorized to be charged to Deposit Account No. 16-1852.

Respectfully submitted,



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**APPENDIX A**

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**Percent Sequence Identity**

GAP Comparison of SEQ ID NOS: 5 and 7, and SEQ ID NOS: 6 and 8

**SUMMARY OF RESULTS:****Polynucleotide**

Sequence	Length	GAP % Identity to each other
SEQ ID NO: 5	720	99.44%
SEQ ID NO: 7	767	99.44%

**Polypeptide**

Sequence	Length	GAP % Identity to each other
SEQ ID NO: 6	238	99.15%
SEQ ID NO: 8	237	99.16%

**GAP Alignments provided on the following pages:**

GAP of SEQ ID NO: 5 vs. SEQ ID NO: 7 begins on page 2

GAP of SEQ ID NO: 6 vs. SEQ ID NO: 8 begins on page 4

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GAP of: BB1410SID5 check: 4302 from: 1 to: 720

to: BB1410sid7 check: 8620 from: 1 to: 767

Symbol comparison table: nwsgapdna.cmp CompCheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000
Quality:	7080	Length:	775
Ratio:	9.833	Gaps:	0
Percent Similarity:	99.438	Percent Identity:	99.438

Match display thresholds for the alignment(s):

| = IDENTITY

: = 5

. = 1

BB1410SID5 x BB1410sid7 November 29, 2005 12:04 ..

```
1 .....atggcggccaatgcgggcggcggtggagcgggaggaggcagcggc 45
   |||||||||||||||||||||||||||||||||||||||||||||||
51 gaggcatggcggccaatgcgggcggcggtggagcgggaggaggcagcggc 100
   |||||||||||||||||||||||||||||||||||||||||||||||
46 agcggcagcgtggctgcgcggcggtgtgccgccccagcggctcgcggtg 95
   |||||||||||||||||||||||||||||||||||||||||||||||
101 agcggcagcgtggctgcgcggcggtgtgccgccccagcggctcgcggtg 150
   |||||||||||||||||||||||||||||||||||||||||||||||
96 gacgccgacgccggagcagatcaggatgctgaaggagctctactacggct 145
   |||||||||||||||||||||||||||||||||||||||||||||||
151 gacgccgacgccggagcagatcaggatgctgaaggagctctactacggct 200
   |||||||||||||||||||||||||||||||||||||||||||||||
146 gcggcatccggtcgcccagctcggagcagatccagcgcacccgccatg 195
   |||||||||||||||||||||||||||||||||||||||||||||||
201 gcggcatccggtcgcccagctcggagcagatccagcgcacccgccatg 250
   |||||||||||||||||||||||||||||||||||||||||||||||
196 ctgcggcagcagcggaagatcgagggcaagaacgtcttctactggttcca 245
   |||||||||||||||||||||||||||||||||||||||||||||||
251 ctgcggcagcagcggaagatcgagggcaagaacgtcttctactggttcca 300
   |||||||||||||||||||||||||||||||||||||||||||||||
246 gaaccacaaggcccgagcgcgcagaagcgcgcctcaccagcctcgacg 295
   |||||||||||||||||||||||||||||||||||||||||||||||
301 gaaccacaaggcccgagcgcgcagaagcgcgcctcaccagcctcgacg 350
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296 tcaacgtgcccgcgcgcggcgcgcgacgccaccaccagccaactcggc 345
    |||||||
351 tcaacgtgcccgcgcgcggcgcgcgacgccaccaccagccaactcggc 400
    |||||||
346 gtcctctcgtgtgtcgtcgccgcgccttcaggcgcgcgccctccctcgcc 395
    |||||||
401 gtcctctcgtgtgtcgtcgccgcgccttcaggcgcgcgccctccctcgcc 450
    |||||||
396 caccctcgggtttatacgcgcgcggccaatggcgcgcgatcggtgtgtgtgc 445
    |||||||
451 caccctcgggtttctacgcgcgcggccaatggcgcgcgatcggtgtgtgtgc 500
    |||||||
446 tggacacgagttccgactggggcagcagcggcgctgccatggccaccgag 495
    |||||||
501 tggacacgagttccgactggggcagcagcggcgctgccatggccaccgag 550
    |||||||
496 acatgcttctcgcaggtcggtgctgtagtacgttcttttctcgggcattg 545
    |||||||
551 acatgcttctcgcaggtcggtgctgtagtacgttcttttctcgggcattg 600
    |||||||
546 cgcgcagtttcacgttcgtacgtacgagttgatcgccggtcggttcacac 595
    |||||||
601 cgcgcagtttcacgttcgtacgtacgagttgatcgccggtcggttcacac 650
    |||||||
596 caccggtatatataactggttaggtacggcggtgcgcgcgcgcaggactac 645
    |||||||
651 caccggtatatataactggttaggtacggcggtgcgcgcgcgcaggactac 700
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646 atgggcggtgacggacacgggcagctcgtcgagtgggccacgcttctcgtc 695
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701 atgggcggtgacggacacgggcagctcgtcgagtgggccacgcttctcgtc 750
    |||||||
696 gtcggacacgataatggcgcgcgcc 720
    |||||||
751 gtcggacacgataatgg..... 767
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